

SEQUENCE LISTING

5 <110> Lunden, Anne

Andersson, Leif

Marklund, Stefan

10

<120> Mutations in the FMO3 gene

15

<130> Ref

20

<160> 20

25 <170> PatentIn version 3.1

<210> 1

30

<211> 20

<212> DNA

35 <213> Artificial Sequence

<220>

40

<223> Primer

<400> 1

gaccatgcag aagagggcag

20

45

<210> 2

<211> 27

50

<212> DNA

<213> Artificial Sequence

55

<220>

<223> Primer

60

<400> 2

cttaaactgt atgtatttca ggaggtt

27

<210> 3
5 <211> 21
<212> DNA
<213> Artificial Sequence
10

<220>
15 <223> Primer

<400> 3
catcatcagc tccagaagtg g 21
20
<210> 4
<211> 21
25 <212> DNA
<213> Artificial Sequence

30
<220>
<223> Primer
35 <400> 4
taaaggcatc aagccatagt t 21

<210> 5
40 <211> 21
<212> DNA
45 <213> Artificial Sequence

<220>
50 <223> Primer

<400> 5
cagaatcctg aggaaagagc c 21
55

<210> 6
60 <211> 20
<212> DNA

<213> Artificial Sequence

5 <220>

<223> Primer

<400> 6

10 attacttgtg ctgcccagcg

20

<210> 7

15 <211> 26

<212> DNA

<213> Artificial Sequence

20

<220>

25 <223> Primer

<400> 7

gatgaatgat attaatgaga aaatgg

26

30

<210> 8

<211> 18

35 <212> DNA

<213> Artificial Sequence

40

<220>

<223> Primer

45 <400> 8

ccggtccac tgggtcag

18

<210> 9

50

<211> 142

<212> DNA

55 <213> Bos taurus

<220>

60

<221> exon

<222> (2) .. (142)

<223>

5

<400> 9

10 g gcc agc att tat cgg tca gtc ttt acc aac tct tcc aaa gag atg aca 49
 Ala Ser Ile Tyr Arg Ser Val Phe Thr Asn Ser Ser Lys Glu Met Thr
 1 5 10 15

15 tgt ttt cca gac ttt cca ttt cct gat gat ttt cct aac ttt atg cac 97
 Cys Phe Pro Asp Phe Pro Phe Pro Asp Asp Phe Pro Asn Phe Met His
 20 25 30

20 aac agc aag ctc cag gaa tat att act atg ttt gcc aaa gaa aag 142
 Asn Ser Lys Leu Gln Glu Tyr Ile Thr Met Phe Ala Lys Glu Lys
 35 40 45

<210> 10

<211> 151

25

<212> DNA

<213> Bos taurus

30

<220>

<221> exon

35

<222> (2) .. (151)

<223>

40

<400> 10

45 c tcc tgg gtg atg agc cgg gtc tgg gat gaa ggc tat cca tgg gac atg 49
 Ser Trp Val Met Ser Arg Val Trp Asp Glu Gly Tyr Pro Trp Asp Met
 1 5 10 15

50 ctg ttt atc act cga ttt gaa aca ttc ctc aag aac acc tta ccg aca 97
 Leu Phe Ile Thr Arg Phe Glu Thr Phe Leu Lys Asn Thr Leu Pro Thr
 20 25 30

55 gtc att tct aac tgg tgg tac atg aag caa atg aac gcc aga ttc aag 145
 Val Ile Ser Asn Trp Trp Tyr Met Lys Gln Met Asn Ala Arg Phe Lys
 35 40 45

55 cac gag 151
 His Glu
 50

60 <210> 11

<211> 313

<212> DNA

5 <213> Bos taurus

<220>

10

<221> exon

<222> (2) .. (313)

15 <223>

<400> 11

20	t	gtg	ttc	aat	gac	gaa	ctc	cca	gct	tgc	att	tta	tgt	ggc	att	gtg	acc	49
		Val	Phe	Asn	Asp	Glu	Leu	Pro	Ala	Cys	Ile	Leu	Cys	Gly	Ile	Val	Thr	
	1					5					10					15		
		att	aag	cca	aat	gtg	aag	gag	ttt	aca	gag	gat	tca	gct	att	ttt	gag	97
25	Ile	Lys	Pro	Asn	Val	Lys	Glu	Phe	Thr	Glu	Asp	Ser	Ala	Ile	Phe	Glu		
			20						25					30				
		gat	ggg	acg	gtg	ttt	aag	gcc	att	gac	tat	gtc	atc	ttt	gca	aca	ggc	145
30	Asp	Gly	Thr	Val	Phe	Lys	Ala	Ile	Asp	Tyr	Val	Ile	Phe	Ala	Thr	Gly		
			35					40					45					
		tat	agt	tat	gcc	tac	ccc	ttc	ctt	gat	gac	tcc	atc	att	aag	agc	aga	193
		Tyr	Ser	Tyr	Ala	Tyr	Pro	Phe	Leu	Asp	Asp	Ser	Ile	Ile	Lys	Ser	Arg	
			50					55					60					
35		gac	aat	gag	gtc	acc	tta	ttt	aaa	ggc	ata	ttc	cca	cct	cca	ctg	gaa	241
	Asp	Asn	Glu	Val	Thr		Leu	Phe	Lys	Gly	Ile	Phe	Pro	Pro	Pro	Leu	Glu	
	65						70				75					80		
40	aag	cca	acc	ttg	gct	gtg	atc	ggc	ctt	gtc	cag	tcc	ctt	gga	gct	gcc	289	
	Lys	Pro	Thr	Leu	Ala	Val	Ile	Gly	Leu	Val	Gln	Ser	Leu	Gly	Ala	Ala		
					85				90						95			
		atc	ccc	act	act	gac	ctg	cag	tct								313	
45	Ile	Pro	Thr	Thr	Asp	Leu	Gln	Ser										
						100												

<210> 12

50

<211> 202

<212> DNA

55 <213> Bos taurus

<220>

60

<221> exon

<222> (2) .. (202)

<223>

5

<400> 12

g ttt ggc aaa agt gat acc ata cag acg gat tat gtt gtt tat atg gat 49
 Phe Gly Lys Ser Asp Thr Ile Gln Thr Asp Tyr Val Val Tyr Met Asp
 10 1 5 10 15
 gag ctt gcc tcc ttc att ggg gca aag ccc aac atc cca tgg ctg ttt 97
 Glu Leu Ala Ser Phe Ile Gly Ala Lys Pro Asn Ile Pro Trp Leu Phe
 20 25 30
 15 ctc aca gat cca aag ttg gca ttg gag gtc tac ttt ggc cct tgc acc 145
 Leu Thr Asp Pro Lys Leu Ala Leu Glu Val Tyr Phe Gly Pro Cys Thr
 35 40 45
 20 cca tac cag ttt agg ctg gtg ggc cca gga aag tgg cca gga gcc aga 193
 Pro Tyr Gln Phe Arg Leu Val Gly Pro Gly Lys Trp Pro Gly Ala Arg
 50 55 60
 aac gcc atc 202
 25 Asn Ala Ile
 .65

<210> 13

30

<211> 714

<212> DNA

35 <213> Bos taurus

<220>

40

<221> Intron

<222> (1) .. (714)

45 <223>

<220>

50

<221> Intron

<222> (1) .. (714)

55 <223>

<400> 13

60 ctcagattgt aagagcatct gtggtaaagg ggatccagaa ttttcatagc aaaatttgac 60
 tttgtgaata cttaaactgt tttagtcttg aatactcctg agtgggacca ttaggggtgac 120

agctatgagc taaattcagc cattcaacaa atagttatca aggatatact tcgcacctga 180
 tagaccacta aatcctgttt cagccctcca tatctcctgc aatatatcat aaaagagaga 240
 5 cccagaaaga ttaaatttca gaggagcttg ggaacacacg gatgtggact tctattttct 300
 agctcataca tcctctaaaa tgtaaggatg ccttccaata ggtggctcta ataaatgact 360
 10 cagccacaca acaactagtc agaagaacta ggctccagtc ctacctctgt cactaatcag 420
 ctcagtggcc atgaattaat aactacaogt gagcaagaga caattcctct acttgtaa at 480
 gtggataaaa atgcctttct cagcagcctt gttgtgttgt ggaatgtcca agtgagatca 540
 15 gtatgaaagt ccttcagtaa aatctacaaa gtactggata atgagcaata atcccccttac 600
 caacaaaagg atcgatgttg atttgcgtgg ataaaaaggt gtgaggcatt ttccctgttc 660
 20 ttgtttctaa aggaagctcg gatagccaca gtcttgtttc tctccctcct ctag 714

<210> 14

25 <211> 1672

<212> DNA

<213> Bos taurus

30

<220>

35 <221> CDS

<222> (18)..(1616)

<223>

40

<220>

45 <221> mRNA

<222> (1)..(1672)

<223>

50

<400> 14

55 attacagaaa ggtaact atg gtg aag aaa gtg gcc atc att gga gca ggc 50
 Met Val Lys Lys Val Ala Ile Ile Gly Ala Gly
 1 5 10
 atc agt ggc ctg gcc tcc atc aga aac tgc cta gaa gag gga ctg gaa 98
 60 Ile Ser Gly Leu Ala Ser Ile Arg Asn Cys Leu Glu Glu Gly Leu Glu
 15 20 25
 ccc acc tgc ttt gag aag ggt gaa gac att ggg ggc ctg tgg aaa ttc 146

	Pro Thr Cys Phe Glu Lys Gly Glu Asp Ile Gly Gly Leu Trp Lys Phe	
	30 35 40	
5	tcg gac cat gta gag gaa ggc agg gcc agc att tat cgg tca gtc ttt Ser Asp His Val Glu Glu Gly Arg Ala Ser Ile Tyr Arg Ser Val Phe	194
	45 50 55	
10	acc aac tct tcc aaa gag atg aca tgt ttt cca gac ttt cca ttt cct Thr Asn Ser Ser Lys Glu Met Thr Cys Phe Pro Asp Phe Pro Phe Pro	242
	60 65 70 75	
15	gat gat ttt cct aac ttt atg cac aac agc aag ctc cag gaa tat att Asp Asp Phe Pro Asn Phe Met His Asn Ser Lys Leu Gln Glu Tyr Ile	290
	80 85 90	
	act atg ttt gcc aaa gaa aag aac ctc ctg aaa tac ata caa ttt aag Thr Met Phe Ala Lys Glu Lys Asn Leu Leu Lys Tyr Ile Gln Phe Lys	338
	95 100 105	
20	aca att gta tcc agt gta aat aag cgt ccc gat ttc caa acc act ggc Thr Ile Val Ser Ser Val Asn Lys Arg Pro Asp Phe Gln Thr Thr Gly	386
	110 115 120	
25	caa tgg gat gtt atc act gaa aag gat ggt aaa aag gaa tca gct gtc Gln Trp Asp Val Ile Thr Glu Lys Asp Gly Lys Lys Glu Ser Ala Val	434
	125 130 135	
30	ttt gat gcc gta atg att tgt tct gga cat cat gtg tac ccc aac ata Phe Asp Ala Val Met Ile Cys Ser Gly His His Val Tyr Pro Asn Ile	482
	140 145 150 155	
	cct aaa gag tcc ttt cca gga ata aaa ctt ttt aaa ggc aaa tgc ttc Pro Lys Glu Ser Phe Pro Gly Ile Lys Leu Phe Lys Gly Lys Cys Phe	530
	160 165 170	
35	cac agc cgg gac tat aaa gaa cca gga atc ttc aag ggg aag cga gtc His Ser Arg Asp Tyr Lys Glu Pro Gly Ile Phe Lys Gly Lys Arg Val	578
	175 180 185	
40	ctg gtg att ggt ctg ggg aac tca ggc tgt gac atc gcc tca gaa ctc Leu Val Ile Gly Leu Gly Asn Ser Gly Cys Asp Ile Ala Ser Glu Leu	626
	190 195 200	
45	agc cac ata gct gaa aaa gtc atc atc agc tcc cga agt ggc tcc tgg Ser His Ile Ala Glu Lys Val Ile Ile Ser Ser Arg Ser Gly Ser Trp	674
	205 210 215	
50	gtg atg agc cgg gtc tgg gat gaa ggc tat cca tgg gac atg ctg ttt Val Met Ser Arg Val Trp Asp Glu Gly Tyr Pro Trp Asp Met Leu Phe	722
	220 225 230 235	
	atc act cga ttt gaa aca ttc ctc aag aac acc tta ccg aca gtc att Ile Thr Arg Phe Glu Thr Phe Leu Lys Asn Thr Leu Pro Thr Val Ile	770
	240 245 250	
55	tct aac tgg tgg tac atg aag caa atg aac gcc aga ttc aag cac gag Ser Asn Trp Trp Tyr Met Lys Gln Met Asn Ala Arg Phe Lys His Glu	818
	255 260 265	
60	aac tac ggc ttg atg cct tta aac agc acc ctg agg aaa gag cct gtg Asn Tyr Gly Leu Met Pro Leu Asn Ser Thr Leu Arg Lys Glu Pro Val	866
	270 275 280	

	ttc aat gac gaa ctc cca gct tgc att tta tgt ggc att gtg acc att	914
	Phe Asn Asp Glu Leu Pro Ala Cys Ile Leu Cys Gly Ile Val Thr Ile	
	285 290 295	
5	aag cca aat gtg aag gag ttt aca gag gat tca gct att ttt gag gat	962
	Lys Pro Asn Val Lys Glu Phe Thr Glu Asp Ser Ala Ile Phe Glu Asp	
	300 305 310 315	
10	ggg acg gtg ttt aag gcc att gac tat gtc atc ttt gca aca ggc tat	1010
	Gly Thr Val Phe Lys Ala Ile Asp Tyr Val Ile Phe Ala Thr Gly Tyr	
	320 325 330	
15	agt tat gcc tac ccc ttc ctt gat gac tcc atc att aag agc aga gac	1058
	Ser Tyr Ala Tyr Pro Phe Leu Asp Asp Ser Ile Ile Lys Ser Arg Asp	
	335 340 345	
20	aat gag gtc acc tta ttt aaa ggc atc ttc cca cct cca ctg gaa aag	1106
	Asn Glu Val Thr Leu Phe Lys Gly Ile Phe Pro Pro Pro Leu Glu Lys	
	350 355 360	
25	cca acc ttg gct gtg atc ggc ctt gtc cag tcc ctt gga gct gcc atc	1154
	Pro Thr Leu Ala Val Ile Gly Leu Val Gln Ser Leu Gly Ala Ala Ile	
	365 370 375	
30	ccc act act gac ctg cag tct cgc tgg gca gta caa gta att aag gga	1202
	Pro Thr Thr Asp Leu Gln Ser Arg Trp Ala Val Gln Val Ile Lys Gly	
	380 385 390 395	
35	aca tgc cct ttg cct tct gtc aag gac atg atg aat gat att gat gaa	1250
	Thr Cys Pro Leu Pro Ser Val Lys Asp Met Met Asn Asp Ile Asp Glu	
	400 405 410	
40	aaa atg ggg aaa aag ctc aaa ttg ttt ggc aaa agt gat acc ata cag	1298
	Lys Met Gly Lys Lys Leu Lys Leu Phe Gly Lys Ser Asp Thr Ile Gln	
	415 420 425	
45	acg gat tat gtt gtt tat atg gat gag ctt gcc tcc ttc att ggg gca	1346
	Thr Asp Tyr Val Val Tyr Met Asp Glu Leu Ala Ser Phe Ile Gly Ala	
	430 435 440	
50	aag ccc aac atc cca tgg ctg ttt ctc aca gat cca aag ttg gca ttg	1394
	Lys Pro Asn Ile Pro Trp Leu Phe Leu Thr Asp Pro Lys Leu Ala Leu	
	445 450 455	
55	gag gtc tac ttt ggc cct tgc acc cca tac cag ttt agg ctg gtg ggc	1442
	Glu Val Tyr Phe Gly Pro Cys Thr Pro Tyr Gln Phe Arg Leu Val Gly	
	460 465 470 475	
60	cca gga aag tgg cca gga gcc aga aac gcc atc ctg acc cag tgg gac	1490
	Pro Gly Lys Trp Pro Gly Ala Arg Asn Ala Ile Leu Thr Gln Trp Asp	
	480 485 490	
65	cgg tta ctg aaa cct atg acg aca aga gtg gtt ggg agt cct ctg aag	1538
	Arg Leu Leu Lys Pro Met Thr Thr Arg Val Val Gly Ser Pro Leu Lys	
	495 500 505	
70	cct tgc tta ttt tgc aac tgg ttc aga cct gtt ctt att tct gtt gta	1586
	Pro Cys Leu Phe Cys Asn Trp Phe Arg Pro Val Leu Ile Ser Val Val	
	510 515 520	
	tca att gct gct ctc att gtg ttg ttc tag ccatcattct atctaggatt	1636

Ser Ile Ala Ala Leu Ile Val Leu Phe
525 530

5 ctgaacatta ctaacaatac ctggaaagaa gcttca 1672

<210> 15

10 <211> 532

<212> PRT

<213> Bos taurus

15

<400> 15

20 Met Val Lys Lys Val Ala Ile Ile Gly Ala Gly Ile Ser Gly Leu Ala
1 5 10 15

25 Ser Ile Arg Asn Cys Leu Glu Glu Gly Leu Glu Pro Thr Cys Phe Glu
20 25 30

Lys Gly Glu Asp Ile Gly Gly Leu Trp Lys Phe Ser Asp His Val Glu
35 40 45

30

Glu Gly Arg Ala Ser Ile Tyr Arg Ser Val Phe Thr Asn Ser Ser Lys
50 55 60

35 Glu Met Thr Cys Phe Pro Asp Phe Pro Phe Pro Asp Asp Phe Pro Asn
65 70 75 80

40 Phe Met His Asn Ser Lys Leu Gln Glu Tyr Ile Thr Met Phe Ala Lys
85 90 95

45 Glu Lys Asn Leu Leu Lys Tyr Ile Gln Phe Lys Thr Ile Val Ser Ser
100 105 110

Val Asn Lys Arg Pro Asp Phe Gln Thr Thr Gly Gln Trp Asp Val Ile
115 120 125

50

Thr Glu Lys Asp Gly Lys Lys Glu Ser Ala Val Phe Asp Ala Val Met
130 135 140

55 Ile Cys Ser Gly His His Val Tyr Pro Asn Ile Pro Lys Glu Ser Phe
145 150 155 160

60 Pro Gly Ile Lys Leu Phe Lys Gly Lys Cys Phe His Ser Arg Asp Tyr
165 170 175

Lys Glu Pro Gly Ile Phe Lys Gly Lys Arg Val Leu Val Ile Gly Leu
 180 185 190

5 Gly Asn Ser Gly Cys Asp Ile Ala Ser Glu Leu Ser His Ile Ala Glu
 195 200 205

10 Lys Val Ile Ile Ser Ser Arg Ser Gly Ser Trp Val Met Ser Arg Val
 210 215 220

15 Trp Asp Glu Gly Tyr Pro Trp Asp Met Leu Phe Ile Thr Arg Phe Glu
 225 230 235 240

Thr Phe Leu Lys Asn Thr Leu Pro Thr Val Ile Ser Asn Trp Trp Tyr
 245 250 255

20 Met Lys Gln Met Asn Ala Arg Phe Lys His Glu Asn Tyr Gly Leu Met
 260 265 270

25 Pro Leu Asn Ser Thr Leu Arg Lys Glu Pro Val Phe Asn Asp Glu Leu
 275 280 285

30 Pro Ala Cys Ile Leu Cys Gly Ile Val Thr Ile Lys Pro Asn Val Lys
 290 295 300

35 Glu Phe Thr Glu Asp Ser Ala Ile Phe Glu Asp Gly Thr Val Phe Lys
 305 310 315 320

Ala Ile Asp Tyr Val Ile Phe Ala Thr Gly Tyr Ser Tyr Ala Tyr Pro
 325 330 335

40 Phe Leu Asp Asp Ser Ile Ile Lys Ser Arg Asp Asn Glu Val Thr Leu
 340 345 350

45 Phe Lys Gly Ile Phe Pro Pro Pro Leu Glu Lys Pro Thr Leu Ala Val
 355 360 365

50 Ile Gly Leu Val Gln Ser Leu Gly Ala Ala Ile Pro Thr Thr Asp Leu
 370 375 380

55 Gln Ser Arg Trp Ala Val Gln Val Ile Lys Gly Thr Cys Pro Leu Pro
 385 390 395 400

60 Ser Val Lys Asp Met Met Asn Asp Ile Asp Glu Lys Met Gly Lys Lys
 405 410 415

Leu Lys Leu Phe Gly Lys Ser Asp Thr Ile Gln Thr Asp Tyr Val Val

12/13

420 425 430

5 Tyr Met Asp Glu Leu Ala Ser Phe Ile Gly Ala Lys Pro Asn Ile Pro
435 440 445

10 Trp Leu Phe Leu Thr Asp Pro Lys Leu Ala Leu Glu Val Tyr Phe Gly
450 455 460

15 Pro Cys Thr Pro Tyr Gln Phe Arg Leu Val Gly Pro Gly Lys Trp Pro
465 470 475 480

20 Gly Ala Arg Asn Ala Ile Leu Thr Gln Trp Asp Arg Leu Leu Lys Pro
485 490 495

25 Met Thr Thr Arg Val Val Gly Ser Pro Leu Lys Pro Cys Leu Phe Cys
500 505 510

30 Asn Trp Phe Arg Pro Val Leu Ile Ser Val Val Ser Ile Ala Ala Leu
515 520 525

Ile Val Leu Phe
530

35 <210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

40 <220>
<223> Primer

45 <400> 16
gatgaaggct atccatggga c

50 <210> 17
<211> 24
<212> DNA

55 <213> Artificial Sequence

60 <220>
<223> Primer

<400> 17
taaaggcatc aagccgtagt tctc 24

5
<210> 18
<211> 18

10 <212> DNA
<213> Artificial Sequence

15
<220>
<223> Primer

20 <400> 18
tgaggaatgt ttcaaatac 18

<210> 19
25 <211> 27
<212> DNA

30 <213> Artificial Sequence

<220>
35 <223> Primer

<400> 19
ggacttagac acacagaaga aaagaag 27

40
<210> 20
<211> 29

45 <212> DNA
<213> Artificial Sequence

50
<220>
<223> Primer

55 <400> 20
gaggtgtgaa attcttattt tttaaatac 29